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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                           Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Run on:
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110:
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113:
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                                                                                                                                                                                                           SPTREMBL_15:*
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Gapop 10.0 , Gapext 0.5
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375
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Copyright (c) 1993 - 2000 Compugen Ltd.
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sp_bacteria:*
sp_fungi:*
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sp_rodent:*
sp_virus:*
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                                                                      sp_organelle:*
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sp_mhc:*
                                                                                                                                  sp_human:*
sp_invertebrate:*
sp_unclassified:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	1.5	14	13	12	11	10	9	80	7	σ	5	4	ω	2	1	Result No.
75	75	75.5	76	77.5	78	78	78	80	80	81	84.5	84.5	95	116.5	124	339	353	375	Score
20.0	20.0	20.1	20.3	20.7	20.8	20.8	20.8	21.3	21.3	21.6	22.5	22.5	25.3	31.1	33.1	90.4	94.1	100.0	Query Match
1670	298	395	411	296	763	763	539	242	242	646	1655	810	637	525	593	666	666	625	Query Match Length DB
S	6	S	S	10	5	G	4	10	10	ν	G	10	10	10	10	10	10	10	HC.
Q23901	Q27944	Q9U2K1	P91419	Q9S709	Q9TXH4	Q22873	Q9NUA2	Q9SBE6	081251	Q9KMZ5	024754	Q9ZWI3	Q03678	Q43358	Q9SEW4	Q9SPL5	Q9SPL4	Q9SPL3	ID
Q23901 dictyosteli	Q27944 aotus trivi	Q9u2k1 caenorhabdi	P91419 caenorhabdi	Q9s709 arabidopsis	. Q9txh4 caenorhabdi	Q22873 caenorhabdi	Q9nua2 homo sapien	Q9sbe6 zea mays su	O81251 zea mays su	Q9kmz5 vibrio chol	Q24754 drosophila	Q9zwi3 cucurbita m	_	Q43358 theobroma c	Q9sew4 juglans reg	Q9sp15 macadamia i	Q9sp14 macadamia i	Q9spl3 macadamia i	Description

RESULT

2

45	44	43	42	41	40	39	38	37	36	35	34	33	32	3 1	30	29	28	27	26	25	24	23	22	21	20
71	71.5	71.5	71.5	72	72	72	72	72.5	73	73	. 73	73	73	73	73.5	73.5	73.5	74	74	74	74	74.5	74.5	74.5	74.5
18.9	19.1	19.1	19.1	19.2			19.2			19.5	19.5	19.5	19.5	19.5	19.6	19.6	19.6	19.7	19.7	19.7	19.7	19.9	19.9	19.9	19.9
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Q9VZ51	Q99621	Q9VZ60	018118	Q03866	Q9SBE9	Q9SBF0	081252	076940	Q9W4J3	Q9V7P3	Q9SBE7	Q9S6Z6	Q9SBE5	081258	Q9VD46	Q9QR71	035540	Q9U9S7	Q9ZTPO	081255	081254	6FAA6Ö	040947	Q9W352	Q99053
•	Q99621 homo sapien	Q9vz60 drosophila	caenorhabd	Q03866 zea mays (m	Q9sbe9 zea mays su	Q9sbf0 zea mays su	O81252 zea mays su	076940 drosophila	Q9w4j3 drosophila	Q9v7p3 drosophila	Q9sbe7 zea mays su	zea	Q9sbe5 zea luxuria	O81258 zea luxuria	Q9vd46 drosophila	Q9qr71 kaposi's sa	O35540 mus musculu	Q9u9s7 dictyosteli		zea mays	O81254 zea mays su	Q9vyj9 drosophila	040947 kaposi's sa	Q9w352 drosophila	Q99053 rattus norv

ALIGNMENTS

1 KRDPQQ 145 KRDPQQ 61 KQSDNP 	Query Match Best Local Similarity Matches 66; Conser	SEQUENCE	PFAM;	INT	SH	7 17														\vdash	1
KRDPOQREYEDCRRHCEQQEPRLQYQCQRRCQEQQRQHGRGGDLMNPQRGGSGRYEEGEE 60	100.0%; Score 375; DB 10; Length 625; imilarity 100.0%; Pred. No. 1.2e-36; ; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	625 AA; 73586 MW; 415808A89D370296 CRC64;	PFAM; PF00546; Seedstore_7s; 1.	INTERPRO; IPRO01113;	HSSP; P02853; 2PHL.	EMBL: AF161885: AAD54246.1:	globulin protein in Macadamia integrifolia.";	Ø	Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;	TISSUE=NUT KERNEL;	SEQUENCE FROM N.A.	NCBI_TaxID=60698;	Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.	Macadamia integrifolia (Macadamia nut). Rikarvota: Viridinlantae: Embryophyta: Tracheophyta: Chermatophyta:	LIN PRECURSOR (FRAGMENT).	(TrEMBLrel. 15,	1.351	(Treustral 13	Q9SPL3 PRELIMINARY; PRT; 625 AA.	Q9SPL3	RESOLD!

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OSSPLA
AC QOOD
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EMBL; AF161884; AAD54245.1; -. INTERROO; IPROOTICE
PFAM: PT. 1 PROOTICE
PFAM: PT. 2 PROOTICE
PFAM: PT. 2 PROOTICE
PFAM: PT. 1 PROO
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=NUT KERNEL;
Marcus J.P., Goulter K.C., Greer
"A family of antimicrobial pepti
globulin protein in Macadamia ir
plant J. 0:0-0(1999).
EMBL; AF161883; AD54244.1;
HSSP; P02853; 2PHL.
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Eukaryota; Viridiplantae; Embryophyta; Trav
Magnoliophyta; eudicotyledons; Proteaceae;
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01-MAY-2000
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Marcus J.P., Goulter K.C.,
Marcus J.P., Goulter K.C.,
TA family of antimicrobial
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnoliophyta; eudicotyledons; Proteaceae; Macadamia
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INTERPRO; IPR001113; -.
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  186
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                                           1 KRDPQQREYEDCRRHCEQQEPRLQYQCQRRCQEQQRQHGRGGDLMNPQRGGSGRYEEGEE
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                                                                                          Similarity
59; Conserv
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                                                                                          Conservative
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                                                                                                                                                                                                        Seedstore_7s; :
AA; 78217 MW;
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AA; 78243 MW;
                                                                                                           90.4%;
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93.98;
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13,
15,
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Last annotation update)
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4; Mismatches
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Query Match
Best Local S
Matches 30
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Q43358; O1-NOV-1996 (TrEMBLrel. (
01-NOV-1996 (TrEMBLrel. (
01-OCT-2000 (TrEMBLrel. 1
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Q9SEW4;
Q1-MAY-2000
Q1-MAY-2000
Q1-OCT-2000
MCHenry L., Fritz P.J.;

"Comparison of the structure and nucleotide sequences of vicilin of cocoa and cotton raise questions about vicilin evolution."; plant Mol. Biol. 18:1173-1176(1992).

EMBL; X62625; CAA44493.1; -.

EMBL; X62626; CAA44494.1; -.

EMBL; X62633; 2PHL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CV. SUNLAND; TISSUE=SOMATIC EMBRYO LINE; Teuber S.S., Jarvis K.C., Peterson W.R., Dandekar A.M., Ansar Teuber S.S., and cloning of a cDNA encoding a vicilin-like "Identification and cloning of a cDNA encoding a vicilin-like Jug r 2, from English walnut kernel (Juglans regia): a major allergen.";
                                                                                                                                                                                                                Theobroma cacao (Cacao).
Eukaryota; Viridiplantae; Embr
Magnoliophyta; eudicotyledons;
Malvales; Malvaceae; Theobroma
                                                                                                                                                                                                                                                                                                        VICILIN PRECURSOR
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Bukaryota; Viridiplantae; Embryophyta; Trachec
Magnoliophyta; eudicotyledons; core eudicots;
Fagales; Juglandaceae; Juglans.
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01-MAY-2000 (TERMBLIEL 13, Last sequence update)
01-CCT-2000 (TERMBLIEL 15, Last annotation update)
VICILIN-LIKE PROTEIN PRECURSOR (FRAGMENT).
                                                                                                                      TISSUE=LEAVES;
MEDLINE=92288309; PubMed=1600151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=51240;
                                                                                                                                                                                            NCBI_TaxID=3641;
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Pred. No. 6.8e
12; Mismatches
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ام. 6.8
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Best Local S
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01-NOV-1996 (TrEMBLrel. 0
01-OCT-2000 (TrEMBLrel. 1
FETAL STORAGE PROTEIN.
Q9ZWI3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BEG1 OR GBL1.
Hordeum vulgare (Barley), (
Eukaryota; Viridiplantae; )
Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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PRODOM; PD081059; -; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERPRO;
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MENDEL; 8553; Horvu;1188;8553.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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PFAM; PF00546; Seeds
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                                                                                                                                                                                                                                                                                                                                          storage protein.
ENCE 637 AA; 72252 MW;
                                                                                                           RHGEGEREE 110
                                                                                                                             RYEEGEEKQ 62
                                                                                                                                                                            QQCVQRCRQERPRYSHARCVQECRDDQQQHGRHEQEEEQGRGRGWHGEGEREEEHGRGRG 101
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M81719; AAA34269.1;
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Embryophyta; Tracheophyta; Spermatophyta;
poales; Poaceae; Hordeum.
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                                                                                                                                                                                                                                                  Score 95; DB
Pred. No. 0.00
12; Mismatches
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Q24754;
01-NOV-1996
01-NOV-1996
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Pterygota; Ne
Ephydroidea;
                                 SEQUENCE FROM N.A.
MEDLINE-94365848; PubMed-8083889;
Newfeld S.J., Tachida H., Yedvobnick B.;
"Drive-selection equilibrium: homopolymer evolution gene mastermind.";
J. Mol. Evol. 38:637-641(1994).
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                                                                                                                                                                                                                               Newfeld S.J., Schmid A.T., Yedvobnick B., "Homopolymer length variation in the Dros J. Mol. Evol. 37:483-495(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 260-762 FROM N.A. MEDLINE-91251140; PubMed=1904096; Newfeld S.J., Smoller D.A., Yedvo
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                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=941111143; PubMed=8283480;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PV100
SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Interspecific comparison
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neoptera; Endopterygota; Diptera; Brachy Missonsophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 01, (TrEMBLrel. 01, (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             810 AA;
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(TrembLrel. 15, Last ann
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Last annotation updat
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Pred. No. 0.044;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A829A3F7542266AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                 obnick B.;
unusually
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dicots; Rosidae; eurosids I;
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Best Local
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                                                                                          081251;
081251;
01-NOV-1998
       GLOBULIN-1 (FRAGMENT).
Zea mays subsp. mays (maize).
Zea mays subsp. mays (maize).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnollophyta; Lillopsida; Poales; Poaceae; Zea.
MCBI_TaxID=4578;
                                                                01-NOV-1998 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                           EMBL; AE004357; AAF96084.1; -. TIGR; VCA0171; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN-EL TOR N16961 / SEROTYPE 01;

MEDLINE-20406833; PubMed-10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwi
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL PROTEIN VCA0171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Newfeld S.J.;
Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; M92914; AAC37201.1; -.
FLYBASE; FB9n0013119; Dvir\mam.
SEQUENCE 1655 AA; 175048 MW; 247D8F8DF0DDDE12 CRC64:
                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                              "DNA sequence of both chromosomes cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                             Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P., McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9KMZ5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9KMZ5;
                                                                                                                                                                                                                                                                                                                                                                   Nature 406:477-483(2000)
                                                                                                                                                                                                                                                                                                                                                                                                     Salzberg S.L., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                    Fraser C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vibrio cholerae
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                                                                                                                                                                                                                                                                                                                                  646 AA; 71064 MW;
                                                                                                                                                                                                   66
                                                                                           (TrEMBLrel.
                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                   21.6%;
28.8%;
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15,
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                                                                   Last sequence update)
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Pred. No. 0.08
13; Mismatches
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Pred. No. 0.09
18; Mismatches
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                                                                  update)
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                                                                                                                                                                                                                                                                                             Length 646
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                                                                                                                                                                                                                                                                                                                                                                                       pathogen Vibrio
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                               Spermatophyta;
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RESULT
Q9NUA2
ID Q91
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O9SBE6:
O1-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
Q9NUA2;
Q9NUA2;
Q1-QCT-2000
                                                                                                                                                                                                       PFAM;
                                                                                                                                                                                                                                        Hilton H., Gaut B.S.;
"Speciation and domestication in maize evidence from the Globulin-1 gene.";
Genetics 0:0-0(1998).
                                                                                                                                                                                                                                                                                              Zea mays subsp. parviglumis.
Eukaryota; Viridiplantae; Embryophyta; Trac
Magnoliophyta; Liliopsida; Poales; Poaceae;
NCBI_TaxID=76912;
                                                                                                                                                                                                                                                                                                                                    GLOBULIN-1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        evidence from the Globulin-1 gene. Genetics 0:0-0(1998).
EMBL; AF064214; AAC31457.1; -.
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                                                                                                                                                                                      SEQUENCE
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"Speciation and domestication in maize
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                                                                                                                                         Local Similarity
nes 22; Conserv
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                                    12
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                                                                                  EEKQSD
                                                                                                                    CRRHCE----QQEPRLQYQCQRRCQEQQRQHGRGGDLMNPQRGGSG-----
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                                                                EEKQKD
                                                                                                 CVRRCEDRPWHQRPRCLEQCREKEREKRQERGRH---ETDDRSGEGSSEDEREREREQEK 96
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                                                                                                                                                                                                                          P50477;
                                                                                                                                                                                                      PF00546; Seedstore_7s;
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                                                                                                                                                                                      242 AA;
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                                                                                                                                         Conservative
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                   PRELIMINARY;
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27856 MW;
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Pred.
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Pred. No.
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ceae; Zea.
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                                                                                                                                                        Length 242;
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                                                                                                                                                                                                                                                             relatives:
                                                                                                                                                                                                                                                                                                                Spermatophyta;
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                                                                                                                    RYEEG
                                                                                                                                      Gaps
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Query Match
Best Local :
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PFAM; PF00098; ZICC...
PFAM; PF00070; DEAD; 1.
PFAM; PF00271; helicase_C; 1.
PFANTS; PR00939; C2HCZNFINGER.
PRINTS; PR00939; C2HCZNFINGER.
PRINTS; PS00039; DEAD_ATP_HELICASE; 1.
PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
PALICASE; ATP-binding; RNA-binding.
PASS AA; 79750 MW; FD5A53BCAF
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gruidl M.E.,
Strome S., B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation updat
ATP-DEPENDENT RNA HELICASE GLH-1.
                                                                                                                                                                                                                                                                        INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 160-763 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUL-1996) to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6239;
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SEQUENCE
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Mammalia; Eutheria;
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01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DJ80804.1 (ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR))
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  Local Similarity
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                                                                                                                                                                                                                            PRO; IPR001878; -. PF00098; zf-CCHC; 4.
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18; Conserv
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                                                                                                                                                                                                                                                                      IPR001650; -.
                                                                                                                                                                                                                                                                                               IPR001410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ., Smith P.A., Bennett K.L.;
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539 I
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55444 MW;
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Primates;
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28
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Score
Pred.
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Catarrhini; Hominidae; Homo
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                                                                                      FD5A53BCA8F9355E CRC64;
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78;
No.
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DB 5;
0.25;
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Matches 22; Conser
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           Q9S709
Q9S709;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2000
T22C5.10.
T17H3.14.
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Q9TXH4;
01-MAY-2000
01-MAY-2000
01-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                     INTERPRO;
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                  PFAM; PF00271; helicase_C; PRINTS; PR01228; EGGSHELL. PROSITE; PS00039; DEAD_ATP Helicase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roussell D.L., Bennett K.L.;
"glh-1, a germ-line putative RNA helicase from Caenorhabditis, four zinc fingers.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad.
[2]
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                                                                                                                                                                                                                                                                                                                                                         ; IPR001410; -.; IPR001650; -.; IPR001878; -.
                                                                                                                                                                                                                                                                        763 AA;
                                (TrEMBLrel.
                                                     (TrEMBLrel.
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 14, Last annotation update)
                                                                          PRELIMINARY;
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                                                      Created)
                                Last sequence update)
Last annotation updat
                                                                                                                                                                                                                            Score 78; DB 5; Pred. No. 0.25;
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Search completed: March
Job time: 1571 sec
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RT "Arabidopsis thaliana chromosome 1 BAC T17H3 sequence.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AC012375; AAR24943 1: -.
DR EMBL; AC012375; AAR24943 1: -.
DR EMBL; AC005916; AAD46002.1; -.
DR EMBL; AC0005916; AAD46002.1; -.
DR FFAM; PF00076; rrm; 1.
DR PFAM; PF000776; rrm; 1.
DR PFAM; PF00642; zf-CCH; 2.
SQ SEQUENCE 296 AA; 34572 MW; F284D29BF68445BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                    Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases. [2]
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                                                                                                                                                                                             215 RRDPSHREFSHRDRDREFYRHGSGKRSSERSERQERDGSRGRRQASPKRGGSPGGGREGS 274
                                                                                                           275
                                                                                                                                                    60 EKQ 62
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                                                                                                           EER 277
                    1,
                                                                                                                                                                                                                                                                                                      20.7%;
                    2001, 16:09:27
                                                                                                                                                                                                                                                                               Score 77.5; DB 10;
Pred. No. 0.11;
9; Mismatches 32;
                                                                                                                                                                                                                                                                                                                           Length 296;
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